#4

SEQUENCE LISTING

<110> Cyclacel

<120> Compositions and Methods for Monitoring the Modification of Modification Dependent Binding Partner Polypeptides

<130> 10069/1062

<140> 09/770102
<141> 2001-01-25

<150> US 60/179283
<151> 2000-01-31

<160> 57

<170> PatentIn version 3.0

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<212> PRT
<213> Unknown

<220>
<223> ADP-ribosylation domain

<220>
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<222> (1)..(17)
<223> ADT-ribosylation site

<400> 1

Met Leu Cys Cys Met Arg Arg Thr Lys Gln Val Glu Lys Asn Asp Asp
1   5   10   15

Asp

<210> 2
<211> 10
<212> PRT
<213> Unknown

<220>
<223> ADP-ribosylation site

<220>
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<223> ADP-ribosylation site

<400> 2

1

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Phe Lys Gln Arg Gln Thr Arg Gln Phe Lys
1               5                   10

<210>   3
<211>   30
<212>   PRT
<213>   Unknown

<220>
<223>   ubiquitination site

<220>
<221>   DOMAIN
<222>   (1)..(30)
<223>   ubiquitination site


<400>   3

Met Phe Gln Ala Ala Glu Arg Pro Gln Glu Trp Ala Met Glu Gly Pro
1               5                   10                  15

Arg Asp Gly Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His
            20                  25                  30

<210>   4
<211>   21
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<213>   Unknown

<220>
<223>   ubiquitination site

<220>
<221>   DOMAIN
<222>   (1)..(21)
<223>   ubiquitination site


<400>   4

His Gly Ser Gly Ala Trp Leu Leu Pro Val Ser Leu Val Lys Arg Lys
1               5                   10                  15

Thr Thr Leu Ala Pro
            20

<210>   5
<211>   10
<212>   PRT
<213>   Unknown

<220>
<223>   O-GlcNAc site

<220>
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<222>  (1)..(10)
<223>  O-GlcNAc site


<400>  5

Gly Thr Thr Ser Thr Ile Gln Thr Ala Pro
1               5               10

<210>  6
<211>  12
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<213>  Unknown

<220>
<223>  O-GlcNAc site

<220>
<221>  DOMAIN
<222>  (1)..(12)
<223>  O-GlcNAc site


<400>  6

Ser Ala Val Ser Ser Ala Asp Gly Thr Val Leu Lys
1               5               10

<210>  7
<211>  18
<212>  PRT
<213>  Unknown

<220>
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<220>
<221>  DOMAIN
<222>  (1)..(18)
<223>  O-GlcNAc site


<400>  7

Asp Ser Ser Thr Asp Leu Thr Gln Thr Ser Ser Ser Gly Thr Val Thr
1               5               10              15

Leu Pro


<210>  8
<211>  12
<212>  PRT
<213>  Unknown

<220>
<223>  O-GlcNAc site
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3

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<220>
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<222>  (1)..(12)
<223>  O-GlcNAc site


<400>  8

Met Ala Gly Gly Pro Ala Asp Thr Ser Asp Pro Leu
1               5                   10

<210>  9
<211>  13
<212>  PRT
<213>  Unknown

<220>
<223>  O-GlcNAc site

<220>
<221>  DOMAIN
<222>  (1)..(13)
<223>  O-GlcNAc site


<400>  9

Ala Gln Thr Ile Thr Ser Glu Thr Pro Ser Ser Thr Thr
1               5                   10

<210>  10
<211>  8
<212>  PRT
<213>  Unknown

<220>
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<220>
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<222>  (1)..(8)
<223>  X at position 3 may be any amino acid


<400>  10

Arg Arg Xaa Arg Arg Xaa Ser Thr
1               5

<210>  11
<211>  5
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<213>  Unknown

<220>
<223>  Consensus sequence
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4

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<220>
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<223>  Consensus sequence, each Xaa is any amino acid


<400>  11

Lys Xaa Xaa Ser Xaa
1               5


<210>  12
<211>  3
<212>  PRT
<213>  Unknown


<220>
<223>  Consensus sequence


<220>
<221>  DOMAIN
<222>  (1)..(3)
<223>  Consensus sequence,  Xaa is any amino acid


<400>  12

Arg Xaa Thr
1


<210>  13
<211>  5
<212>  PRT
<213>  Unknown


<220>
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<220>
<221>  DOMAIN
<222>  (1)..(5)
<223>  Consensus sequence, each Xaa is any amino acid


<400>  13

Arg Xaa Xaa Ser Xaa
1               5


<210>  14
<211>  4
<212>  PRT
<213>  Unknown


<220>
<223>  Consensus sequence
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<220>
<221>  DOMAIN
<222>  (1)..(4)
<223>  Consensus sequence, each Xaa is any amino acid


<400>  14

Xaa Ser Arg Xaa
1


<210>  15
<211>  8
<212>  PRT
<213>  Unknown


<220>
<223>  Consensus sequence


<220>
<221>  DOMAIN
<222>  (1)..(8)
<223>  Consensus sequence, each Xaa is any amino acid


<400>  15

Xaa Arg Xaa Xaa Ser Xaa Arg Xaa
1                   5


<210>  16
<211>  6
<212>  PRT
<213>  Unknown


<220>
<223>  Consensus sequence


<220>
<221>  DOMAIN
<222>  (1)..(6)
<223>  Consensus sequence, each Xaa is any amino acid


<400>  16

Xaa Arg Xaa Xaa Ser Xaa
1                   5


<210>  17
<211>  6
<212>  PRT
<213>  Unknown


<220>
<223>  Consensus sequence
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6

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<220>
<221>  DOMAIN
<222>  (1)..(6)
<223>  Consensus sequence


<400>   17

Ser Glu Leu Ser Arg Arg
1                   5

<210>  18
<211>  6
<212>  PRT
<213>  Unknown

<220>
<223>  Consensus sequence

<220>
<221>  DOMAIN
<222>  (1)..(6)
<223>  Consensus sequence, each Xaa is any amino acid


<400>   18

Xaa Ser Xaa Xaa Ser Xaa
1                   5

<210>  19
<211>  5
<212>  PRT
<213>  Unknown

<220>
<223>  Consensus sequence

<220>
<221>  DOMAIN
<222>  (1)..(5)
<223>  Consensus sequence, each Xaa is any amino acid


<400>   19

Xaa Ser Xaa Glu Xaa
1               5

<210>  20
<211>  7
<212>  PRT
<213>  Unknown

<220>
<223>  Consensus sequence
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<220>
<221>  DOMAIN
<222>  (1)..(7)
<223>  Consensus sequence,   each Xaa is any amino acid


<400>  20

Xaa Ser Xaa Xaa Xaa Ser Xaa
1               5

<210>  21
<211>  9
<212>  PRT
<213>  Unknown

<220>
<223>  Consensus sequence

<220>
<221>  DOMAIN
<222>  (1)..(9)
<223>  Consensus sequence


<400>  21

Gly Ser Ser Lys Ser Lys Pro Lys Asp
1               5

<210>  22
<211>  9
<212>  PRT
<213>  Unknown

<220>
<223>  Consensus sequence

<220>
<221>  DOMAIN
<222>  (1)..(9)
<223>  Consensus sequence


<400>  22

Gly Cys Ile Lys Ser Lys Arg Lys Asp
1               5

<210>  23
<211>  9
<212>  PRT
<213>  Unknown

<220>
<223>  Consensus sequence
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<220>
<221>  DOMAIN
<222>  (1)..(9)
<223>  Consensus sequence


<400>  23

Gly Cys Ile Lys Ser Lys Glu Asp Lys
1               5

<210>  24
<211>  9
<212>  PRT
<213>  Unknown

<220>
<223>  Consensus sequence

<220>
<221>  DOMAIN
<222>  (1)..(9)
<223>  Consensus sequence


<400>  24

Gly Cys Val Gln Cys Lys Asp Lys Glu
1               5

<210>  25
<211>  9
<212>  PRT
<213>  Unknown

<220>
<223>  Consensus sequence

<220>
<221>  DOMAIN
<222>  (1)..(9)
<223>  Consensus sequence


<400>  25

Gly Cys Thr Leu Ser Ala Glu Asp Lys
1               5

<210>  26
<211>  9
<212>  PRT
<213>  Unknown

<220>
<223>  Consensus sequence
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9

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<220>
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<222>  (1)..(9)
<223>  Consensus sequence


<400>  26

Gly Cys Ile Lys Ser Lys Arg Lys Asp
1                   5

<210>  27
<211>  9
<212>  PRT
<213>  Unknown

<220>
<223>  Consensus sequence

<220>
<221>  DOMAIN
<222>  (1)..(9)
<223>  Consensus sequence


<400>  27

Gly Cys Val Gln Cys Lys Asp Lys Glu
1                   5

<210>  28
<211>  9
<212>  PRT
<213>  Unknown

<220>
<223>  Consensus sequence

<220>
<221>  DOMAIN
<222>  (1)..(9)
<223>  Consensus sequence


<400>  28

Gly Cys Thr Leu Ser Ala Glu Asp Lys
1                   5

<210>  29
<211>  4
<212>  PRT
<213>  Unknown

<220>
<223>  Consensus sequence
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<220>
<221>  DOMAIN
<222>  (1)..(4)
<223>  Consensus sequence, Xaa is any amino acid


<400>  29

Asn Xaa Ser Thr
1

<210>  30
<211>  4
<212>  PRT
<213>  Unknown

<220>
<223>  C-terminal sequence

<220>
<221>  SITE
<222>  (1)..(4)
<223>  C-terminal sequence


<400>  30

His Ser Thr Val
1

<210>  31
<211>  92
<212>  DNA
<213>  Artificial

<220>
<223>  Synthetic primer

<220>
<221>  misc_feature
<222>  (1)..(92)
<223>  Synthetic primer


<400>  31
gggggggagct ctgggaggcg gaggtggagg gctgatgcgc cagctgcagg atgaagttga      60

agaactggaa caggaaaact ggcatctgca ga                                     92


<210>  32
<211>  96
<212>  DNA
<213>  Artificial

<220>
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<223> Synthetic primer .

<220>
<221> misc_feature
<222> (1)..(96)
<223> Synthetic primer

<400> 32
cccccctcga gttattaaac ttcggcttcc aggcactgaa cttcacgcag cagacgggca   60

acttcgttct gcagatgcca gttttcctgt tccagt   96

<210> 33
<211> 37
<212> PRT
<213> Unknown

<220>
<223> Coiled-coil sequence

<220>
<221> DOMAIN
<222> (1)..(37)
<223> Coiled coil sequence

<400> 33

Leu Met Arg Gln Leu Gln Asp Glu Val Glu Glu Leu Glu Gln Glu Asn
1   5   10   15

Trp His Leu Gln Asn Glu Val Ala Arg Leu Leu Arg Glu Val Gln Cys
            20   25   30

Leu Glu Ala Glu Val
        35

<210> 34
<211> 37
<212> PRT
<213> Unknown

<220>
<223> Coiled coil sequence

<220>
<221> DOMAIN
<222> (1)..(37)
<223> Coiled coil sequence

.<400> 34

Arg Met Arg Gln Leu Glu Asp Arg Val Glu Glu Leu Arg Glu Gln Asn
1   5   10   15

Trp His Leu Ala Asn Gln Val Ala Arg Leu Arg Gln Arg Val Cys Glu
          20   25   30

Leu Lys Ala Arg Val
         35

<210> 35
<211> 80
<212> DNA
<213> Artificial

<220>
<223> Synthetic primer

<220>
<221> misc_feature
<222> (1)..(80)
<223> Synthetic primer

<400> 35
gtaccgctag ctcttacaag ggtattgctc agttggagca ggaaatcgcc caattagaac   60

aagaaaatgc acaacttgaa   80

<210> 36
<211> 73
<212> DNA
<213> Artificial

<220>
<223> Synthetic primer

<220>
<221> misc_feature
<222> (1)..(61)
<223> Synthetic primer

<400> 36
gggcatcgat ttcctgctca agctgagcga tctcttgttc aagttgtgca ttttcttgtt   60

ctaattgggc gat   73

<210> 37
<211> 31
<212> PRT
<213> Unknown

<220>
<223> Sequence for cloning

<220>
<221> DOMAIN

13

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<222>  (1)..(31)
<223>  Sequence for cloning


<400>  37

Tyr Lys Gly Ile Ala Gln Leu Glu Gln Glu Ile Ala Gln Leu Glu Gln
1               5                   10                  15

Glu Asn Ala Gln Leu Glu Gln Glu Ile Ala Gln Leu Glu Gln Glu
            20                  25                  30

<210>  38
<211>  38
<212>  PRT
<213>  Unknown

<220>
<223>  Coiled coil sequence

<220>
<221>  DOMAIN
<222>  (1)..(38)
<223>  Coiled coil sequence


<400>  38

Tyr Lys Gly Ile Cys Gln Leu Arg Gln Arg Ile Ala Gln Leu Arg Gln
1               5                   10                  15

Arg Asn Ala Gln Leu Arg Gln Arg Ile Ala Gln Leu Arg Gln Arg Ile
            20                  25                  30

Ala Gln Leu Arg Gln Arg
        35

<210>  39
<211>  36
<212>  PRT
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<220>
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<220>
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<222>  (1)..(36)
<223>  Synthetic peptide


<400>  39

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly
1               5                   10                  15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
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14

Asp Val Leu Asp
        35

<210> 40
<211> 36
<212> PRT
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<220>
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<220>
<221> PEPTIDE
<222> (1)..(36)
<223> Synthetic peptide

<400> 40

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly
1   5   10   15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20   25   30

Asp Val Leu Asp
        35

<210> 41
<211> 33
<212> DNA
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<220>
<223> Synthetic primer

<220>
<221> misc_feature
<222> (1)..(33)
<223> Synthetic primer

<400> 41
gggatccata tgccagaccc cgcggcgcac ctg   33

<210> 42
<211> 33
<212> DNA
<213> Artificial

<220>
<223> Synthetic primer

<220>

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<223>  Synthetic primer


<400>  42
ggaattcgggg cactgctgtt ggggcaggcc tcc                              33


<210>  43
<211>  23
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<220>
<223>  Synthetic primer

<220>
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<222>  (1)..(23)
<223>  Synthetic primer


<400>  43
gggggcccag agtgaagttc agc                                          23


<210>  44
<211>  23
<212>  DNA
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<220>
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<220>
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<223>  Synthetic primer


<400>  44
gggggcccga gcccccgcg tac                                           23


<210>  45
<211>  23
<212>  DNA
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<220>
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<223>  Synthetic primer
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<400> 45
gggggcccaa ccagctctat aac   23

<210> 46
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Synthetic primer

<220>
<221> misc_feature
<222> (1)..(23)
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<400> 46
ggggatccgc gagggggcag ggc   23

<210> 47
<211> 36
<212> PRT
<213> Artificial

<220>
<223> Synthetic peptide

<220>
<221> PEPTIDE
<222> (1)..(36)
<223> Synthetic peptide

<400> 47

Arg Cys Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly
1   5   10   15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            20   25   30

Asp Val Leu Asp
        35

<210> 48
<211> 6
<212> PRT
<213> Unknown

<220>
<223> Cleavage site

<220>
<221> SITE
<222> (1)..(6)
<223> Xaa is any amino acid

<400> 48

Trp Leu Glu His Asp Xaa
1   5

<210> 49
<211> 5
<212> PRT
<213> Unknown

<220>
<223> Cleavage site

<220>
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<222> (1)..(5)
<223> Cleavage site, each Xaa is any amino acid

<400> 49

Asp Glu Xaa Asp Xaa
1   5

<210> 50
<211> 6
<212> PRT
<213> Unknown

<220>
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<220>
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<222> (1)..(6)
<223> Cleavage site, Xaa is any amino acid

<400> 50

Leu Val Glu Xaa Asp Xaa
1   5

<210> 51
<211> 5
<212> PRT
<213> Unknown

<220>
<223> Cleavage site

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<220>
<221>  SITE
<222>  (1)..(5)
<223>  Cleavage site, Xaa is any amino acid


<400>  51

Ile Glu Gly Arg Xaa
1                  5


<210>  52
<211>  8
<212>  PRT
<213>  Unknown

<220>
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<220>
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<223>  Cleavage site,  each Xaa is any amino acid


<400>  52

Glu Asn Xaa Tyr Xaa Gln Ser Gly
1                  5


<210>  53
<211>  5
<212>  PRT
<213>  Artificial

<220>
<223>  Tag peptide

<220>
<221>  PEPTIDE
<222>  (1)..(5)
<223>  Tag peptide


<400>  53

Arg Tyr Ile Arg Ser
1                  5


<210>  54
<211>  6
<212>  PRT
<213>  Artificial

<220>
<223>  Tag peptide
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<220>
<221>  PEPTIDE
<222>  (1)..(6)
<223>  Tag peptide


<400>  54

Asp Thr Tyr Arg Tyr Ile
1                   5


<210>  55
<211>  6
<212>  PRT
<213>  Artificial

<220>
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<220>
<221>  PEPTIDE
<222>  (1)..(6)
<223>  Tag peptide


<400>  55

Thr Asp Phe Leu Tyr Lys
1                   5

<210>  56
<211>  9
<212>  PRT
<213>  Artificial

<220>
<223>  Tag peptide

<220>
<221>  PEPTIDE
<222>  (1)..(9)
<223>  Tag sequence


<400>  56

Glu Glu Glu Glu Tyr Met Pro Met Glu
1                   5


<210>  57
<211>  11
<212>  PRT
<213>  Artificial

<220>
<223>  Tag peptide
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<220>
<221>   PEPTIDE
<222>   (1)..(11)
<223>   Tag sequence


<400>   57

Lys Pro Pro Thr Pro Pro Pro Glu Pro Glu Thr
1               5               10
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